

BLASTX ALIGNMENT OF SEQ ID NO: 4 LEUCINE-RICH REPEAT PROTEIN-LIKE POLYPEPTIDE
(IDENTIFIED AS LRR PROTEIN-LIKE) WITH HUMAN GARP PROTEIN PRECURSOR PROTEIN SEQ
ID NO: 19

Query: Leucine-rich repeat-like protein (SEQ ID 4)
Sbjct: Human Garp protein precursor protein gi|5031707 ref|NP_005503.1| glycoprotein A repetitions predominant precursor; garpin >sp|Q14392|GARP HUMAN GARP PROTEIN PRECURSOR (GARPIN) >pir||S42799 garp precursor - human emb|CAA80847.1| (Z24680) garp [Homo sapiens] (SEQ ID NO: 19)
length = 662
Score = 822 (289.4 bits), Expect = 4.9e-81, P = 4.9e-81
Identities = 245/637 (38%), Positives = 328/637 (51%)
Query: 267 CKLVGGADCRGQSLASVPSLPPHARMLTLDANPLKTLWNHSLQPYPLSLHSCHL 446
CK+V C+ L VPS LPP L L N L+++ L Y L L L + +
Sbjct: 26 CKWVDKVKSCQVLGILLQVPSTLPPDTETLIDSGNQLRSILASPLGFTYALRHLDISTNEI 85
Query: 447 ERISRGAFQEQGHLRSVLGDNCISENYEETAALHALPGLRRIDLSGNALTEDMALML 626
+ GAFQ HL L L N L+ +A L LP + LIDSGN+L + +L
Sbjct: 86 SFLQPGAFQALTHLEHLHLAHNRMLAMATASAGGLGPLPRVTSIDLSGNSLYSGLLERLL 145
Query: 627 QNLSSLRVS LAGNTIMRLDDSVFEGLERLRELDLQRYIFEEGGAFDGLAELRHMLA 806
SL ++SLA N++ RL F + L +LDL N + +IE GAF+GL L HNL+
Sbjct: 146 GEAPSLHTLSLAENSLTRLTRHTFRDMPALAEQLDHSNVLMDIEDGAFEGLPRLTHINTS 205
Query: 807 FNNLPCIVDFGLTRLRVILNVSYNVLEMF-LATGGEAFELLETLDLSHNQLFPPLLPQYS 983
N+L CI DF L +LRVL++S N +E F A+ +A F+L LDL N+LL FP L
Sbjct: 206 RNSLTCTISDFSLQQLRVLDLSCNSIEAFQTASQPAEFQLTWLDLRNKLLHFPDLAALP 265
Query: 984 KLRITLLRDNNMGFYRDLVNTSSPRENVAQFLAVDG-NVTNITTVSLWEEFSSSDIADLR 1160
+L L L NN+ R T P++ +G + ++ S L+ L
Sbjct: 266 RLITYLNL-SNNL--IR--LPTGPRQDSKGIHAPSEGSALPLSAPS--GNASGRPLSQLL 318
Query: 1161 FIDMSQNFQYLPDGFRLKMPSLSHLNIHONCLMTLHIREHEPPGALTELDLSHNQISEL 1340
LD+S N+ + +PD FL + SL LNL +NCL T R L IDLSHN L L
Sbjct: 319 NIDLSYNEIELIPDSFLEHLTSLCFLNLSRNCLRTFEARRLGSLPCIMLIDLSHNALETL 378
Query: 1341 HLAPGLASCLGSLRLFNLSNQLLGVPPGILFANARNITTLIDMSHNQISLCPPLPAASDRV 1520
L A LGSILR L N L +PP FAN ++ L++ N++S C P D G
Sbjct: 379 ELG---ARALGSLRTLLIQGNALRDLPPYTFANLASLQRLNLQGNRVSPCGGP---DEPG 432

Fig. 1A

BLASTX ALIGNMENT OF SEQ ID NO: 4 LEUCINE-RICH REPEAT PROTEIN-LIKE POLYPEPTIDE
(IDENTIFIED AS LRR PROTEIN-LIKE) WITH HUMAN GARP PROTEIN PRECURSOR PROTEIN SEQ
ID NO: 19

Query: 1521 PPSCVDFRNMAISLSLSLEGCGALPDCPFGQTSITYLDISSNWG--VINGSLAPLODV 1694
P CV F + SLRSLSL + L F T LT LDSSN G V G+L L+
Sbjct: 433 PSGCVAFSGITSLRSLSLVDNEIELLRAGAFHTPLTELDLSSNPGLEVAIGALGGLE-- 490

Query: 1695 APMLOVLSLRNMGHSSFMALDFSGFNLRLDLGNCPLPIPRFGGSLAETLDLRNS 1874
L+VL+L+ GL + +D F L+ L+L+ N L P + +++LE LDLR NS
Sbjct: 491 -ASLEVLALQNGNL--MVLQVDLPFCFICKRLNLAENRLSHLPAMTQAVSLEVLDLRNS 547

Query: 1875 LTALPQKAVSEQLSRGLRTIYLSNPYDCCGVGWMGALQ-H-GQTVADWAM-VTCNLSSK 2045
+ LP A+ L LR +YL NP CCG +GW A Q H G+ D + C SS+
Sbjct: 548 FSLPGSAMGG-LETSLRRLYLQGNPLSCCG-NGWLAQQLHQGRVDVDATQDPLICRFSSQ 605

Query: 2046 IIRVTELPGGVPRDCKWERL-DLGILY-LVLILPSC--LTLVACTVI 2177
L P DC+ L ++ L+ L IL S LT L AC +
Sbjct: 606 --EEVSLSHVRPEDECKGGLKNINILITFLIVSAILLTTLAACCV 651

FIG. 1B

09672221.092700

BLASTX ALIGNMENT OF SEQ ID NO: 4 LEUCINE-RICH REPEAT PROTEIN-LIKE POLYPEPTIDE
(IDENTIFIED AS LRR PROTEIN-LIKE) WITH HUMAN INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN COMPLEX ACID LABILE SUBUNIT PROTEIN SEQ ID NO: 20

Query: Leucine-rich repeat-like protein (SEQ ID 4)
 Sbjct: Human sp|O02833|ALS_PAPPA insulin-like growth factor binding protein complex acid labile chain precursor (ALS)
 >pir||JC5239 insulin-like growth factor acid-labile chain - baboon (SEQ ID NO: 20)
 Length = 605

Score = 294 (103.5 bits), Expect = 1.1e-21, P = 1.1e-21
Identities = 158/510 (30%), Positives = 228/510 (44%)

```

Query:      78  PRSAALAEAGAPGDADPREPPAPAGAA-ALDML-----LPLMLCLGFHFL 212
            PRS   E G PG+   P   PA  A + D E+   LP + G   L
Subject:    22  PRSLGAEPTGE--AEGPACATCACSYDENVELSVFCSSRLTRLPLDGIPTGTQAL 79

```

Query: 213 TVGMRNRSGTATAAQGVCKLVGAADCRGQSLASV - PSSLPHPARM - LTIDANPLKLT 383
+ N S AA + + L + + G L S + P + L + L L + N L + + L
Sbjct: 80 WLDNNLISSIPAAFRNLSSLA - FLNLQGGQLGSLPEQALGLENLCHLTLERNQRLST 137

Query: 384 MNHSLQPYPLLESLHSCHLERISGAFQEOGHRSVLVGDNCISENVEETAAALHALP 563
+ P L L L + L R+ G F+ G+L L LG N L+ + AA L
Sbjct: 138 AVGTFAVTPALALGLSNRLSRLEDGLFEGLGNIWDNLGWNLSLAVLPD---AAFRGLG 194

Query: 564 GLRRLDSGNALTEEMALMLQNLSSLRVS LAGNTIMRLDDSVFEGELERLELDLQRY 743
 GLR L L+GN L AL L+ LR + L+ N + + +vF L RL++L L RN
 Sbjct: 195 GLRELVLAGNRLAYLQPALF-SGLAELELDLSRNALRAIKANVFQPLRLQKLYLDRL 25

Query: 744 IFEIEGAFDGLAELRLHNLAFNNLPCTVD--F-GLTRLRVLNVSINVLEWFLAIGGEAA 91
I + GAF GL LR L+L+ N + +++ F GL LRVL +S+N + E
Sbjct: 254 IAAVAPGAFGLKALRWLDLSHNRVAGLIEDTFPGLGLRVLRLSHNAIASLRPRIFEDL 31

```

Query:      915 FELETLIDLSHNQJ-LFFEDLLPQYSKRTLLLRDNNMGFYRDDLYNTSSPREMVAQFL-LV 10
           LE L L HN++ L +L L L D+N L V FL L
Sbjct:      314 HFLEELQGLHNRIROLAERSFEGLGQLEVLTL-DHNQ-----LQEVK-----VGAFLGLT 36

```

Query: 1086 DGNVTNITTVSLWE--EFSSSDLADLRFLDMSQNFQYLRPDGFLRKMPSLSHLNLHQNC 12
+ V N++ L E L L L + + + L L L N L
Sbjct: 363 NVAVMNLGNCRLNLPQVFRGLGKLSHLIEGSCLGRIKPHTFAGLSGLRRLFLKONG 42

```

Query:      1260  MTLPIREHEPPGALTELDLSHQLSLHLAPLASCGLSLRLFNLSNQNLGVPPEGLFAN 14
              + + + L EDDL+ NQL+ HL L LG L LS N+L +P
Sbjct:      423  VGLIEQSLWGALTELDLTSNQLT-HLPQLFQGLGKLEYLLSHNRRLAELPADALGP 48

```

Query: 1440 ARNITTLDMSHNOISLCPPLPAASDRVGPPSCYDFRMMASLRSLSEGGGLGAL 1598
+ LD+SHN++ P ++G ++ RN SLR++ + GL L
Sbjct: 481 LQRAFWLDVSHNRLEALPGSLIAS-LGRLRYINLRNN-SLRITTPQPPGLERL 531

FIG. 2

Abstract

BLASTX ALIGNMENT OF SEQ ID NO: 4 LEUCINE-RICH REPEAT PROTEIN-LIKE POLYPEPTIDE (IDENTIFIED AS LRR PROTEIN-LIKE) WITH HUMAN GLYCOPROTEIN V PROTEIN SEQ ID NO: 21

Query: Leucine-rich repeat-like protein (SEQ ID 4)
 Sbjct: gi|4758460 ref|NP_004479.1| glycoprotein V (platelet) >sp|P40197|GPV HUMAN PLATELET GLYCOPROTEIN V PRECURSOR (GPV) (CD42d) >pir||A60164 platelet membrane glycoprotein V precursor - human >pir||A47507 platelet membrane glycoprotein V precursor - human emb|CAA80637.1| (Z23091) platelet glycoprotein V precursor [Homo sapiens] >gb|AAA03069.1| (L11238) platelet membrane glycoprotein V [Homo sapiens] (SEQ ID NO: 21)
 length = 560

Score = 273 (96.1 bits), Expect = 2.8e-20, Sum P(2) = 2.8e-20
 Identities = 127/386 (32%), Positives = 177/386 (45%)

Query: 837 GLTRLRVLNVSVLEWFLATGGEA-AFELETLDSLHNOQLFFP-ILPQYSKRLTLR 1007
 G+T L+ L +S + + +A G + +L+TL LS N++ P LL + L L L
 Sbjct: 72 GMTVLIQRLMISDSHIS-AVAPGTFSDLIKIKTLRLSRNKITHLPGALIDKWLLEQLFL- 129

Query: 1008 DNNMGFYRDLVNTSSPREMVAQFLVDGNVTNITTVSLWEEFSSDLADIPLDMSQNOF 1187
 D+N R + + + Q L ++ N + SL+ ++L +L+ LD+S N
 Sbjct: 130 DHNA--LRGIDQNMFPQKLVNLQELALNQNQLDFLPASLF-----TNLENLKLDDLSGNNL 182

Query: 1188 QYLPDGFRLKMPSLSHLNLHONCMTLHIREHEPPGALTELDLSHNOQLSELHLAPGLASC 1367
 +LP G L L L LH N L++L GALTDL N + +APG
 Sbjct: 183 THLPKGLLGAQAKLERLLHSHNRLVSLDGLINSGLALTELDQPHRNHIRST--APGAFDR 240

Query: 1368 LGSRLRFNLSSNQLGVPPGLFANARNITTLDMSHNOISLCPPLAASDRVGPSCVDFRN 1547
 L+L LS N L +P LF ++ N+T L + N L LP V F
 Sbjct: 241 LPNLSSLTSLSRNHLAFLPSALFLHSHNLTLLTLFENP--LAELPG-----VLFGGE 288

Query: 1548 MASLRSLSEGGGLGALPDCPFQGTSLTYLD--LSSNWGVL--NGSLAPLDVAPMLQVL 1715
 M L+ L L L LP F+ S L YL LS L G+ L + LQVL
 Sbjct: 289 MGLQELWLNRTQLRTLPAAAFRNLSRLRYLGVTLSPRLSALPGAFQGLGE---LQVL 344

Query: 1716 SLRNMGLHSSFMALDFSGFGNLRDLDSGNCLPIFPR--FGSLALETLDLRNSLTALP 1889
 +L + GL + L G G LR + L N L PR F +LE++ L N L LP
 Sbjct: 345 ALHSNGLTALPDGL-LRGLGKLRQVSLRRNRLRALPRALFRNLSSLESVQLDHNQLETLF 403

Query: 1890 QKAVSEQLSRGLRTIYLSQNPYDC-CGVD--GWGALQH 1994
 V L R L + L N + C CG+ GW OH
 Sbjct: 404 GD-VFGALPR-LTEVLLGHNSWRCDCGLGPFLLGW-LRQH 439

FIG. 3

09672221.092700

BLASTX ALIGNMENT OF SEQ ID NO: 4 LEUCINE-RICH REPEAT PROTEIN-LIKE POLYPEPTIDE
(IDENTIFIED AS LRR PROTEIN-LIKE) WITH WD-40 DOMAIN CONTAINING INSULIN-LIKE
GROWTH FACTOR BINDING PROTEIN SEQ ID NO: 22

Query: Leucine-rich repeat-like protein (SEQ ID 4)
Sbjct: sp|R85888|R85888 WD-40 domain-contg. insulin-like growth factor binding protein (SEQ ID NO: 22)
Length = 605

Score = 293 (103.1 bits), Expect = 7.3e-22, P = 7.3e-22
Identities = 141/467 (30%), Positives = 208/467 (44%)

Query: 198 GFHFLTVGWRNSGTATAAGVCYCKLVGAADCRGQSLASV-PSSLPPHARM--LTLDAN 368
G L + N S AA Q + L G + +G L S+ P +L + L L+ N
Sbjct: 75 GTQALMLDGNNTSSVPPAFQNLSSL--GFLNLQGGQLGLEPQALLGLENLCHLHLERN 132

Query: 369 PLKTLMNHSLQPPYLLLESLSHSCHLERISRGAFQEQGHLSVLVGDNCISENVEETAA 548
L++L + P L SL L + L R+ G F+ G L L LG N L+ + AA
Sbjct: 133 QLRSLALGTFATHPALASLGLSNRRLSRLLEDGLFEGLSIMDLNLGWNLSLAVLPD--AA 189

Query: 549 LHALPGLRLDLSGNALTEDMALMLQNLSSLSVSLAGNTIMRLDDSVFEGELRLRLD 728
L LR L L+GN L AL L+ LR + L+ N + + +VF L RL++L
Sbjct: 190 FRGLGSLRELVLAGNRLAYLQPALF-SGLAEIARELDLSRNALRAIKANVFVQLPRLQKLY 248

Query: 729 LQENYIFEIEGAFDGLAEIRHINLAFNNLPCIVD--F-GLTRRLVNLVSYNVLFWFIAT 899
L RN I + GAF GL LR L+L+ N + +++ F GL LRVL +S+N +
Sbjct: 249 LDRNLIAAVAPGAFGLKALKALRWLDLSHNRVAGLLEDTFPGILLRLVRLSHNALIASLRPR 308

Query: 900 GGEAAFELETLDLSHNQL--LFFPLLQYSKLRTLLLRDNNM-----GFYRDLYNTSSPR 1058
+ LE L L HN++ L +L L L N + G + L N +
Sbjct: 309 TFKDLHFLEELQGHNRIRQLAERSFEGLGQLEVLTLDHNOQEYKAGAFGLTNVA--- 365

Query: 1059 EMVAQFLLVVDGNVTNITTVSLMEEFSSSDLDLRLFLDMSQNFQYLPDGLRKMPSLSHL 1238
+ + GN +L E+ L L L + + + L L
Sbjct: 366 -----VMNLSGNCLR---NLPEQYFRG-LGKLHSLHLEGSCLGRIRPHTFTGLSGLRRL 415

Query: 1239 NLHQNCIMTLHIREHEPPGALTELDLSHNQLSLHLAPGLASCIGSLRLFNLSNQLLGV 1418
L N L+ + + L ELDL+ NQL+ HL L LG L LS N+L +
Sbjct: 416 FLKDNGLVGIIEGSLWGLAEILLEDLTNSQLT--HLPHRLFGGLGKLEYLLLSRRRLAEL 473

Query: 1419 PPGLFANARNITFLDMSHNQISLCPLPASDRVGPSPCVDFRNMAISLSLSEGGGLGAL 1598
P + LD+SHN++ P + +G + RN SLR+ + + GL L
Sbjct: 474 PADALGPLQRAFWLVDVSHNRLEALPNSLIAP-LGRRLYLSLRNN-SLRFTTPQPPGLERL 531

FIG. 4

0915722221.092700